

H: Robinson

1653

#9
Raw listing

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/068,377

DATE: 02/02/2000
TIME: 09:31:32

Input Set: I068377.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

P.S.

ENTERED

1 <110> APPLICANT: Lasky, Laurence A.
2 Dowbenko, Donald J.
3 <120> TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage Furrow-Associated
4 Proteins (PSTPIPs)
5 <130> FILE REFERENCE: P1066P2
6 <140> CURRENT APPLICATION NUMBER: US/09/068,377
7 <141> CURRENT FILING DATE: 1999-05-08
8 <150> EARLIER APPLICATION NUMBER: US 08/938,300
9 <151> EARLIER FILING DATE: 1997-09-29
10 <150> EARLIER APPLICATION NUMBER: US 08/798,419
11 <151> EARLIER FILING DATE: 1997-02-07
12 <160> NUMBER OF SEQ ID NOS: 73
13 <210> SEQ ID NO 1
14 <211> LENGTH: 415
15 <212> TYPE: PRT
16 <213> ORGANISM: Mus Musculus
17 <400> SEQUENCE: 1
18 Met Met Ala Gln Leu Gln Phe Arg Asp Ala Phe Trp Cys Arg Asp
19 1 5 10 15
20 Phe Thr Ala His Thr Gly Tyr Glu Val Leu Leu Gln Arg Leu Leu
21 20 25 30
22 Asp Gly Arg Lys Met Cys Lys Asp Val Glu Glu Leu Leu Arg Gln
23 35 40 45
24 Arg Ala Gln Ala Glu Glu Arg Tyr Gly Lys Glu Leu Val Gln Ile
25 50 55 60
26 Ala Arg Lys Ala Gly Gly Gln Thr Glu Met Asn Ser Leu Arg Thr
27 65 70 75
28 Ser Phe Asp Ser Leu Lys Gln Gln Thr Glu Asn Val Gly Ser Ala
29 80 85 90
30 His Ile Gln Leu Ala Leu Ala Leu Arg Glu Glu Leu Arg Ser Leu
31 95 100 105
32 Glu Glu Phe Arg Glu Arg Gln Lys Glu Gln Arg Lys Lys Tyr Glu
33 110 115 120
34 Ala Ile Met Asp Arg Val Gln Lys Ser Lys Leu Ser Leu Tyr Lys
35 125 130 135
36 Lys Thr Met Glu Ser Lys Lys Ala Tyr Asp Gln Lys Cys Arg Asp
37 140 145 150
38 Ala Asp Asp Ala Glu Gln Ala Phe Glu Arg Val Ser Ala Asn Gly
39 155 160 165
40 His Gln Lys Gln Val Glu Lys Ser Gln Asn Lys Ala Lys Gln Cys
41 170 175 180
42 Lys Glu Ser Ala Thr Glu Ala Glu Arg Val Tyr Arg Gln Asn Ile
43 185 190 195
44 Glu Gln Leu Glu Arg Ala Arg Thr Glu Trp Glu Gln Glu His Arg

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45          200          205          210
46      Thr Thr Cys Glu Ala Phe Gln Leu Gln Glu Phe Asp Arg Leu Thr
47          215          220          225
48      Ile Leu Arg Asn Ala Leu Trp Val His Cys Asn Gln Leu Ser Met
49          230          235          240
50      Gln Cys Val Lys Asp Asp Glu Leu Tyr Glu Glu Val Arg Leu Thr
51          245          250          255
52      Leu Glu Gly Cys Asp Val Glu Gly Asp Ile Asn Gly Phe Ile Gln
53          260          265          270
54      Ser Lys Ser Thr Gly Arg Glu Pro Pro Ala Pro Val Pro Tyr Gln
55          275          280          285
56      Asn Tyr Tyr Asp Arg Glu Val Thr Pro Leu Ile Gly Ser Pro Ser
57          290          295          300
58      Ile Gln Pro Ser Cys Gly Val Ile Lys Arg Phe Ser Gly Leu Leu
59          305          310          315
60      His Gly Ser Pro Lys Thr Thr Pro Ser Ala Pro Ala Ala Ser Thr
61          320          325          330
62      Glu Thr Leu Thr Pro Thr Pro Glu Arg Asn Glu Leu Val Tyr Ala
63          335          340          345
64      Ser Ile Glu Val Gln Ala Thr Gln Gly Asn Leu Asn Ser Ser Ala
65          350          355          360
66      Gln Asp Tyr Arg Ala Leu Tyr Asp Tyr Thr Ala Gln Asn Ser Asp
67          365          370          375
68      Glu Leu Asp Ile Ser Ala Gly Asp Ile Leu Ala Val Ile Leu Glu
69          380          385          390
70      Gly Glu Asp Gly Trp Trp Thr Val Glu Arg Asn Gly Gln Arg Gly
71          395          400          405
72      Phe Val Pro Gly Ser Tyr Leu Glu Lys Leu
73          410          415
74      <210> SEQ ID NO 2
75      <211> LENGTH: 2100
76      <212> TYPE: DNA
77      <213> ORGANISM: Mus Musculus
78      <400> SEQUENCE: 2
79      caatatttca agctataacca agcatacaat caactccaag cttatgcccc 50
80      agaagaagcg gaaggtctcg agcggcgcca attttaatca aagtgggaat 100
81      attgctgata gctcattgtc cttcactttc actaacagta gcaacgggtcc 150
82      gaacctcata acaactcaaa caaattctca agcgctttca caaccaattg 200
83      cctcctctaa cgttcatgat aacttcatga ataatgaaat cacggctagt 250
84      aaaattgatg atggtaataa ttcaaaacca ctgtcacctg gttggacgga 300
85      ccaaactgcg tataacgcgt ttggaatcac tacagggatg tttaatacca 350
86      ctacaatgga tgatgtatat aactatctat tcgatgatga agatacccca 400
87      ccaaacccaa aaaaagaggg tgggtcgacc cacgcgtccg gtccttctct 450
88      catttcgctg ctgattctag ccccaaacaa aacaggttga gcctttttcc 500
89      tcctccggca gttgcctctg gcttgtggct gccttctgag cgtttcagac 550
90      ggcgcgggct gggagtggga gggaggcct gggctagccg cgctgggact 600
91      gggacgtgct cctggctcct ggcccatgct cagccctgct tgaagcagga 650
92      ttgctagcat ttgacacaac gcccttggag gatgatggcc cagctgcagt 700
93      tccgagatgc cttctggtgc agggacttca cggcccacac agggatatgag 750
94      gtgctactgc agaggctgct ggacggcagg aagatgtgca aggatgtgga 800

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95      ggagctgctc agacagaggg cccaggcgga ggagaggtac ggggaaggagc 850
96      tgggtgcagat tgcacgcaag gctggtggcc agacagagat gaattccctg 900
97      aggacctcct ttgactccct gaagcagcaa acagagaatg tgggcagtgc 950
98      acacatccag ctggccctgg cctgcggtga ggagctgcgg agcctggagg 1000
99      agttccgaga gagacagaaa gagcagcgga agaagtatga ggccatcatg 1050
100     gaccgtgtcc agaagagcaa gttgtcgctc tacaagaaga ccatggagtc 1100
101     caagaaggca tatgaccaga agtgcaggga tgcagatgat gctgagcagg 1150
102     ccttcgagcg tgtgagtgcc aatggccacc agaagcaagt agaaaagagc 1200
103     cagaacaaag ccaagcagtg caaggagtca gccacagagg cagaaagagt 1250
104     gtacaggcaa aatatcgaac aactggagag agcgaggacc gagtgggagc 1300
105     aggagcaccg gactacctgt gaggccttcc agttgcagga gtttgaccgg 1350
106     ctcaccatcc tccgcaatgc cctgtgggtg cactgtaacc agctctccat 1400
107     gcagtgtgtc aaggatgatg agctctatga ggaagtgcgg ctgacccttg 1450
108     agggctgtga tgtggaaggt gacatcaatg gcttcatcca gtccaagagc 1500
109     actggcagag agccccagc tccggtgcct tatcagaact actatgacag 1550
110     ggaggtgacc cactgattg gcagccctag catccagccc tccctgcggtg 1600
111     tgataaagag gttctctggtg ctgtacatg gaagtcccaa gaccacacct 1650
112     tctgtcctctg ctgtctccac agagactctg actcccaccc ctgagcggaa 1700
113     tgagttggtc tacgcatcca tcgaagtgcg gccgaccagc ggaacaccta 1750
114     actcatcagc ccaggactac cgggcactct acgactacac tgcacagaat 1800
115     tctgatgagc tggacatttc cgcgggagac atcctggcgg tcatcctgga 1850
116     aggggaggat ggctggtgga ctgtggagcg gaacggacaa cgtggctttg 1900
117     tccctgggtc gtacttgag aagctctgag gaaaggctag cagtctccac 1950
118     atacctccgc cctgactgtg aggtcaggac tgtttcttcc catcaccgcc 2000
119     caggcctcac ggggccagaa ccaagcccgg tgggtgctggg catgggctgg 2050
120     gtgctggcta ctctcaataa atgtctccca gaaggaaaaa aaaaaaaaaa 2100

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121 <210> SEQ ID NO 3

122 <211> LENGTH: 48

123 <212> TYPE: PRT

124 <213> ORGANISM: Mus Musculus

125 <400> SEQUENCE: 3

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126      Leu Tyr Asp Tyr Thr Ala Gln Asn Ser Asp Glu Leu Asp Ile Ser
127      1                5                10                15
128      Ala Gly Asp Ile Leu Ala Val Ile Leu Glu Gly Glu Asp Gly Trp
129      20                25                30
130      Trp Thr Val Glu Arg Asn Gly Gln Arg Gly Phe Val Pro Gly Ser
131      35                40                45
132      Tyr Leu Arg
133      48

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134 <210> SEQ ID NO 4

135 <211> LENGTH: 50

136 <212> TYPE: PRT

137 <213> ORGANISM: Homo sapien

138 <400> SEQUENCE: 4

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139      Leu Tyr Gln Tyr Ile Gly Gln Asp Val Asp Glu Leu Ser Phe Asn
140      1                5                10                15
141      Val Asn Glu Val Ile Glu Ile Leu Ile Glu Asp Ser Ser Gly Trp
142      20                25                30
143      Trp Lys Gly Arg Leu His Gly Gln Glu Gly Leu Phe Pro Gly Asn
144      35                40                45

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145      Tyr Val Glu Lys Ile
146                      50
147 <210> SEQ ID NO 5
148 <211> LENGTH: 50
149 <212> TYPE: PRT
150 <213> ORGANISM: Homo sapien
151 <400> SEQUENCE: 5
152      Leu Tyr Asp Tyr Gln Glu Lys Ser Pro Arg Glu Val Thr Met Lys
153      1                      5                      10                      15
154      Lys Gly Asp Ile Leu Thr Leu Leu Asn Ser Thr Asn Lys Asp Trp
155                      20                      25                      30
156      Trp Lys Val Glu Val Asn Asp Arg Gln Gly Phe Val Pro Ala Ala
157                      35                      40                      45
158      Tyr Val Lys Lys Leu
159                      50
160 <210> SEQ ID NO 6
161 <211> LENGTH: 50
162 <212> TYPE: PRT
163 <213> ORGANISM: Homo sapien
164 <400> SEQUENCE: 6
165      Leu Tyr Asp Tyr Gln Gly Glu Gly Ser Asp Glu Leu Ser Phe Asp
166      1                      5                      10                      15
167      Pro Asp Asp Ile Ile Thr Asp Ile Glu Met Val Asp Glu Gly Trp
168                      20                      25                      30
169      Trp Arg Gly Gln Cys Arg Gly His Phe Gly Leu Phe Pro Ala Asn
170                      35                      40                      45
171      Tyr Val Lys Leu Leu
172                      50
173 <210> SEQ ID NO 7
174 <211> LENGTH: 48
175 <212> TYPE: PRT
176 <213> ORGANISM: Homo sapien
177 <400> SEQUENCE: 7
178      Leu Tyr Asp Tyr Gln Ala Ala Gly Asp Asp Glu Ile Ser Phe Asp
179      1                      5                      10                      15
180      Pro Asp Asp Ile Ile Thr Asn Ile Glu Met Ile Asp Asp Gly Trp
181                      20                      25                      30
182      Trp Arg Gly Val Cys Lys Gly Arg Tyr Gly Leu Phe Pro Ala Asn
183                      35                      40                      45
184      Tyr Val Glu
185                      48
186 <210> SEQ ID NO 8
187 <211> LENGTH: 8
188 <212> TYPE: PRT
189 <213> ORGANISM: Artificial Sequence
190 <220> FEATURE:
191 <221> NAME/KEY: Artificial Sequence
192 <222> LOCATION: 1-8
193 <223> OTHER INFORMATION: Amino acid epitope tag
194 <400> SEQUENCE: 8

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195      Asp Tyr Lys Asp Asp Asp Asp Lys
196      1              5              8
197      <210> SEQ ID NO 9
198      <211> LENGTH: 33
199      <212> TYPE: DNA
200      <213> ORGANISM: Artificial Sequence
201      <220> FEATURE:
202      <221> NAME/KEY: Artificial Sequence
203      <222> LOCATION: 1-33
204      <223> OTHER INFORMATION: Synthetic oligonucleotide probe
205      <400> SEQUENCE: 9
206      cgcgatcca ccatgatggc ccagctgcag ttc 33
207      <210> SEQ ID NO 10
208      <211> LENGTH: 45
209      <212> TYPE: DNA
210      <213> ORGANISM: Artificial Sequence
211      <220> FEATURE:
212      <221> NAME/KEY: Artificial Sequence
213      <222> LOCATION: 1-45
214      <223> OTHER INFORMATION: Synthetic oligonucleotide probe
215      <400> SEQUENCE: 10
216      gtacgcgtcg actcacttgt catcgtcgtc cttgtagtcg agctt 45
217      <210> SEQ ID NO 11
218      <211> LENGTH: 18
219      <212> TYPE: DNA
220      <213> ORGANISM: Artificial Sequence
221      <220> FEATURE:
222      <221> NAME/KEY: Artificial Sequence
223      <222> LOCATION: 1-18
224      <223> OTHER INFORMATION: Synthetic oligonucleotide probe
225      <400> SEQUENCE: 11
226      tgcctttctc tccacagg 18
227      <210> SEQ ID NO 12
228      <211> LENGTH: 36
229      <212> TYPE: DNA
230      <213> ORGANISM: Artificial Sequence
231      <220> FEATURE:
232      <221> NAME/KEY: Artificial Sequence
233      <222> LOCATION: 1-36
234      <223> OTHER INFORMATION: Synthetic oligonucleotide probe
235      <400> SEQUENCE: 12
236      ctcccttgagg ttctactagt gggggctggt gtccctg 36
237      <210> SEQ ID NO 13
238      <211> LENGTH: 39
239      <212> TYPE: DNA
240      <213> ORGANISM: Artificial Sequence
241      <220> FEATURE:
242      <221> NAME/KEY: Artificial Sequence
243      <222> LOCATION: 1-39

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Please Note: <223> OTHER INFORMATION: Synthetic oligonucleotide probe
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

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VERIFICATION SUMMARY
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Line ? Error/Warning

Original Text

515 W "N" or "Xaa" used: Feature required

Pro Xaa Xaa Pro